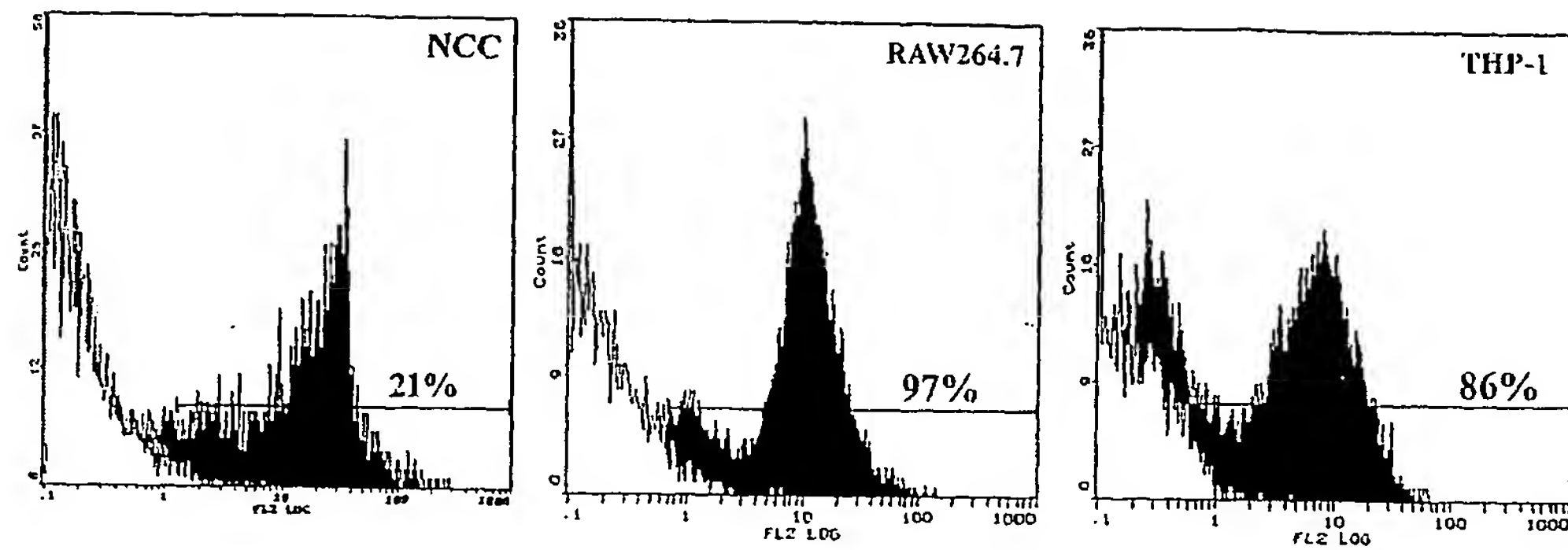


Figures 1A - 1B

A



B

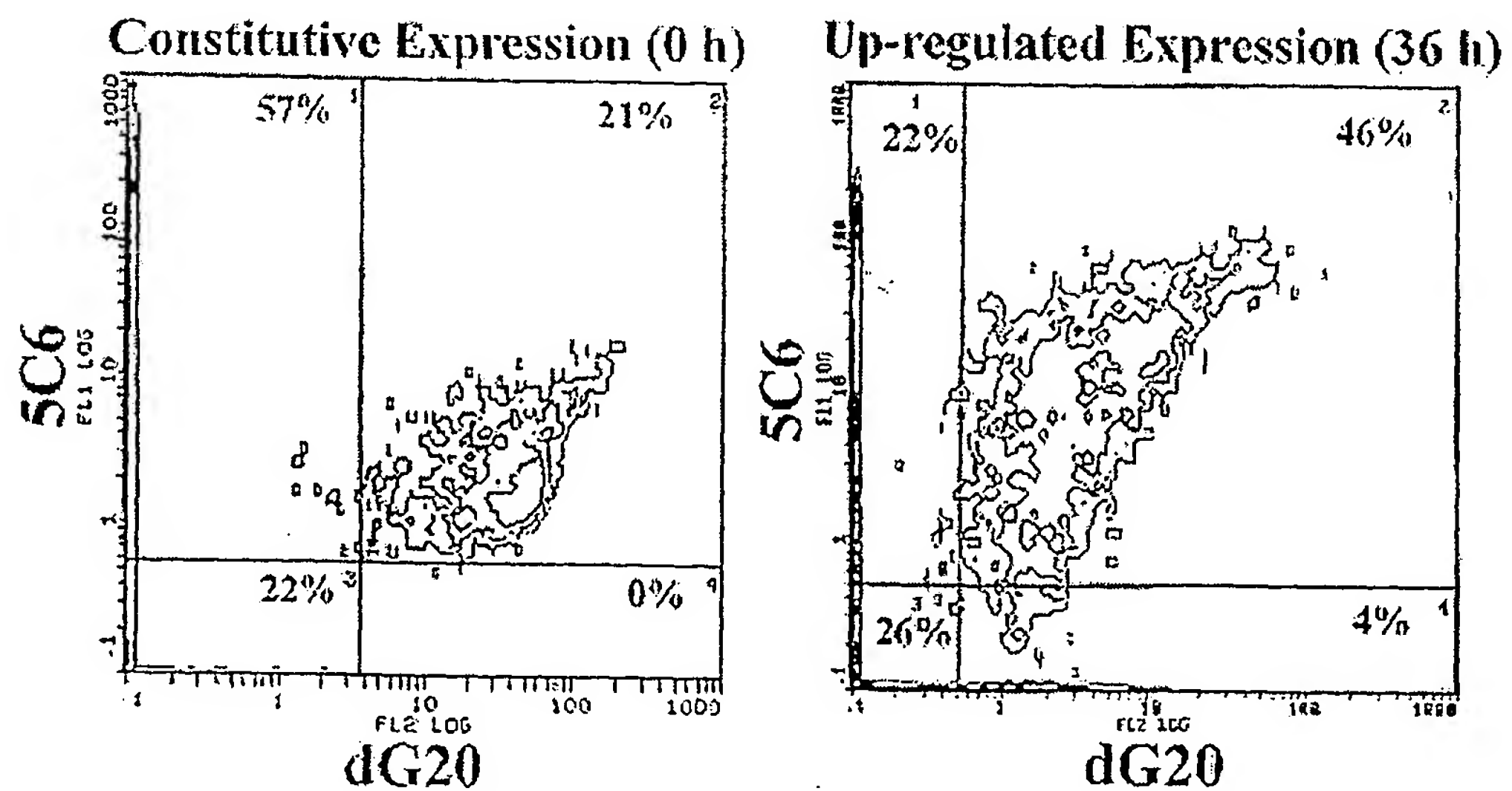
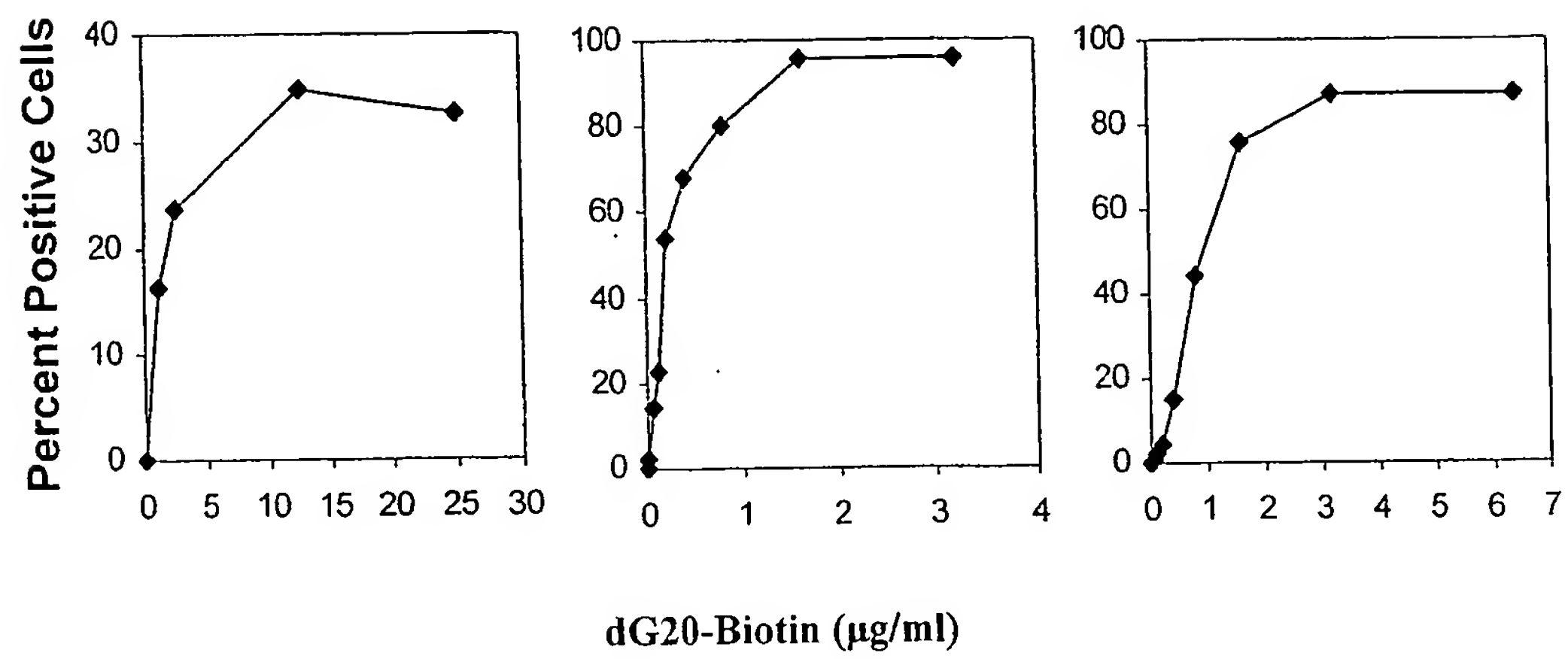
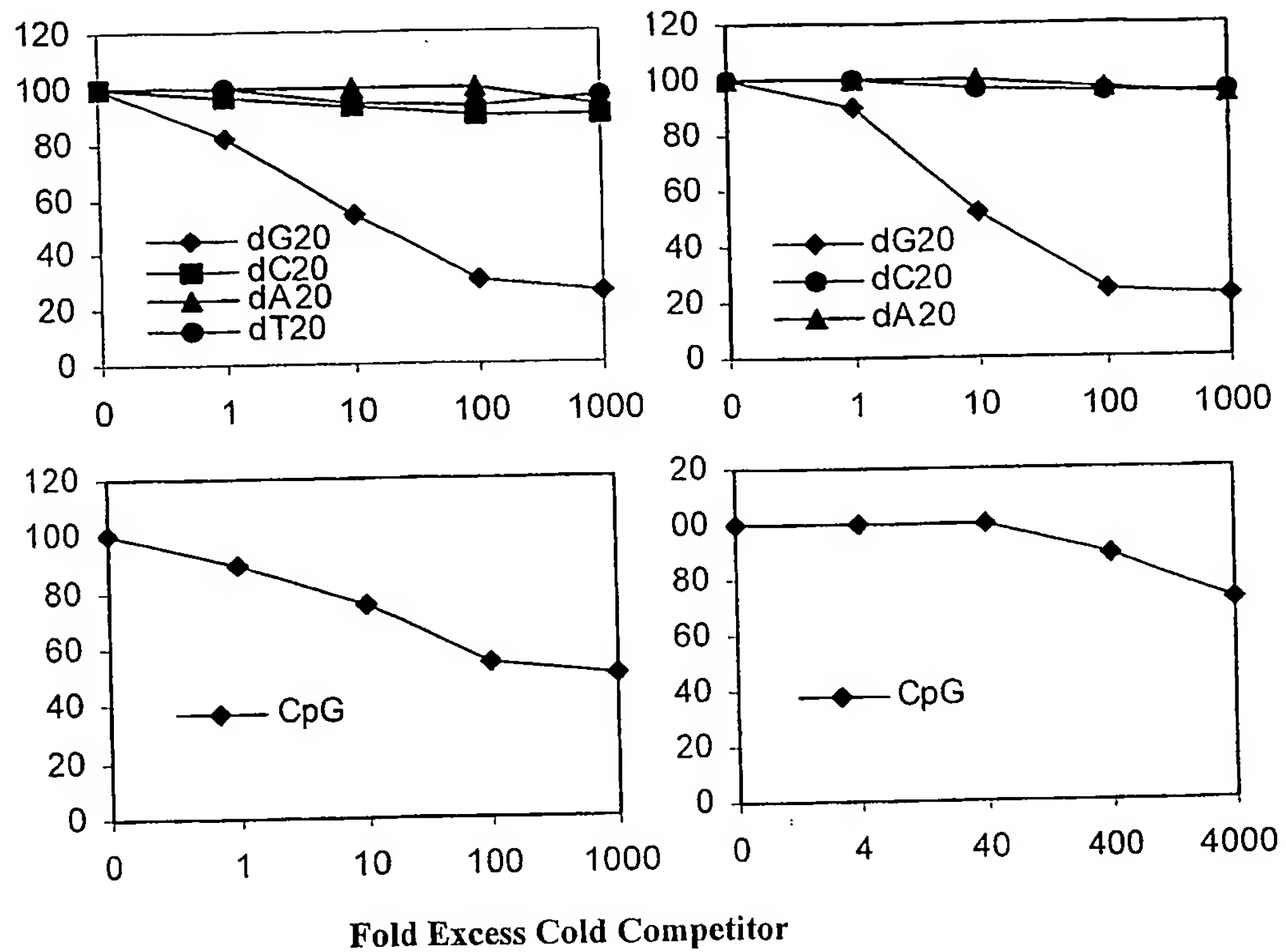
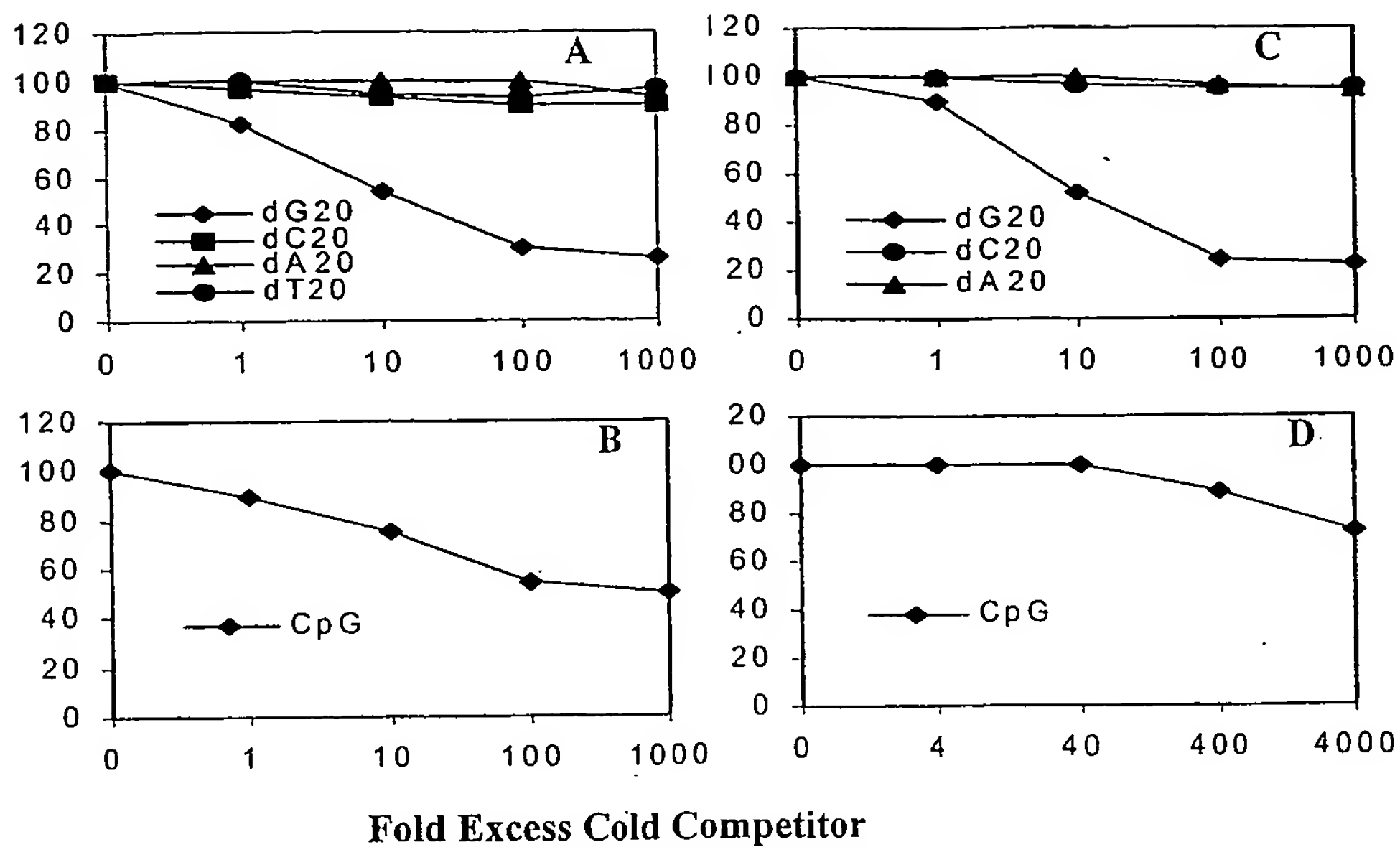


Figure 2

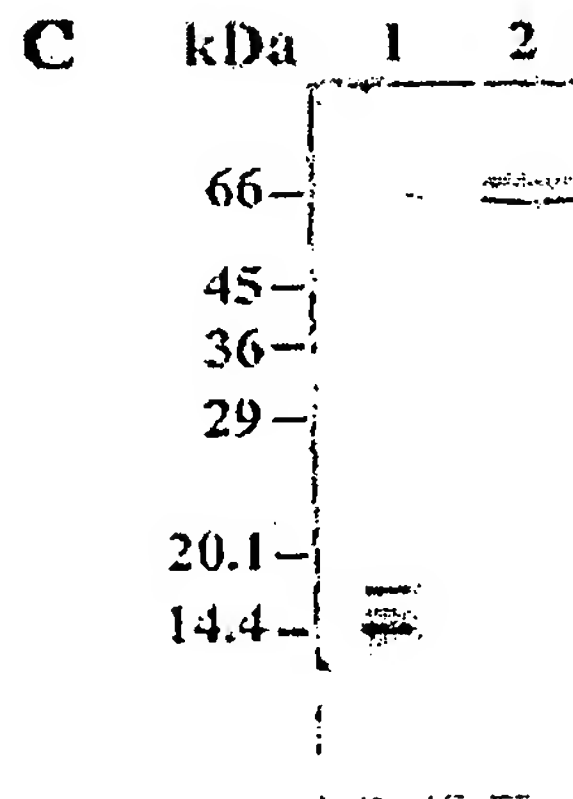
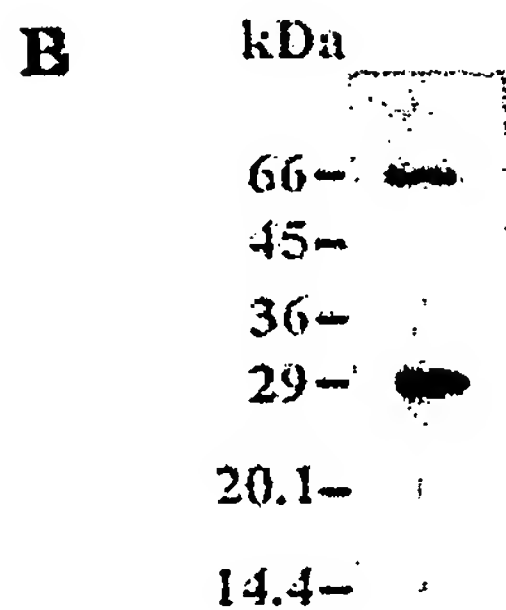
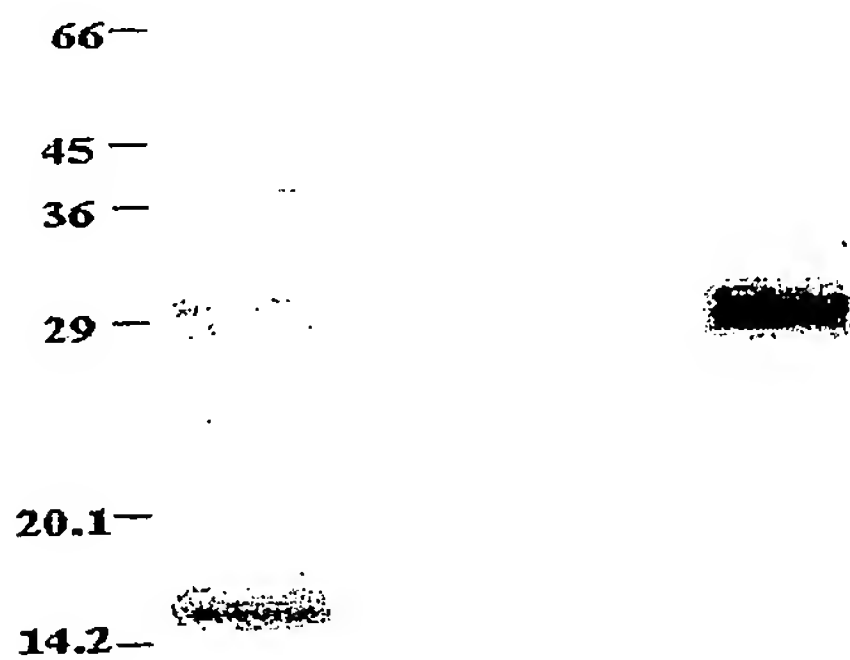
Figures 3A - 3D



Figures 4A - 4C



A 1 2 3 4 5 6



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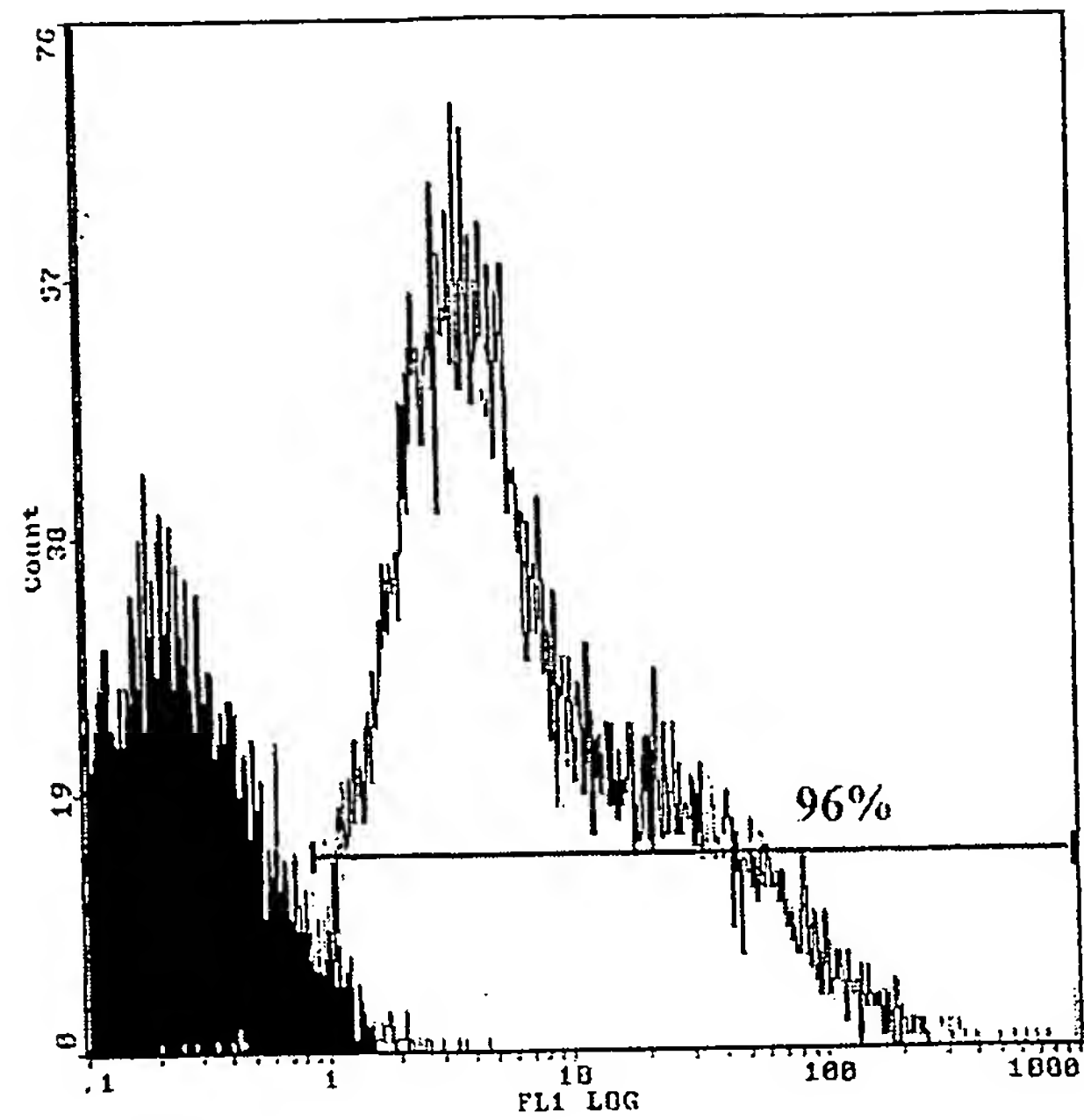
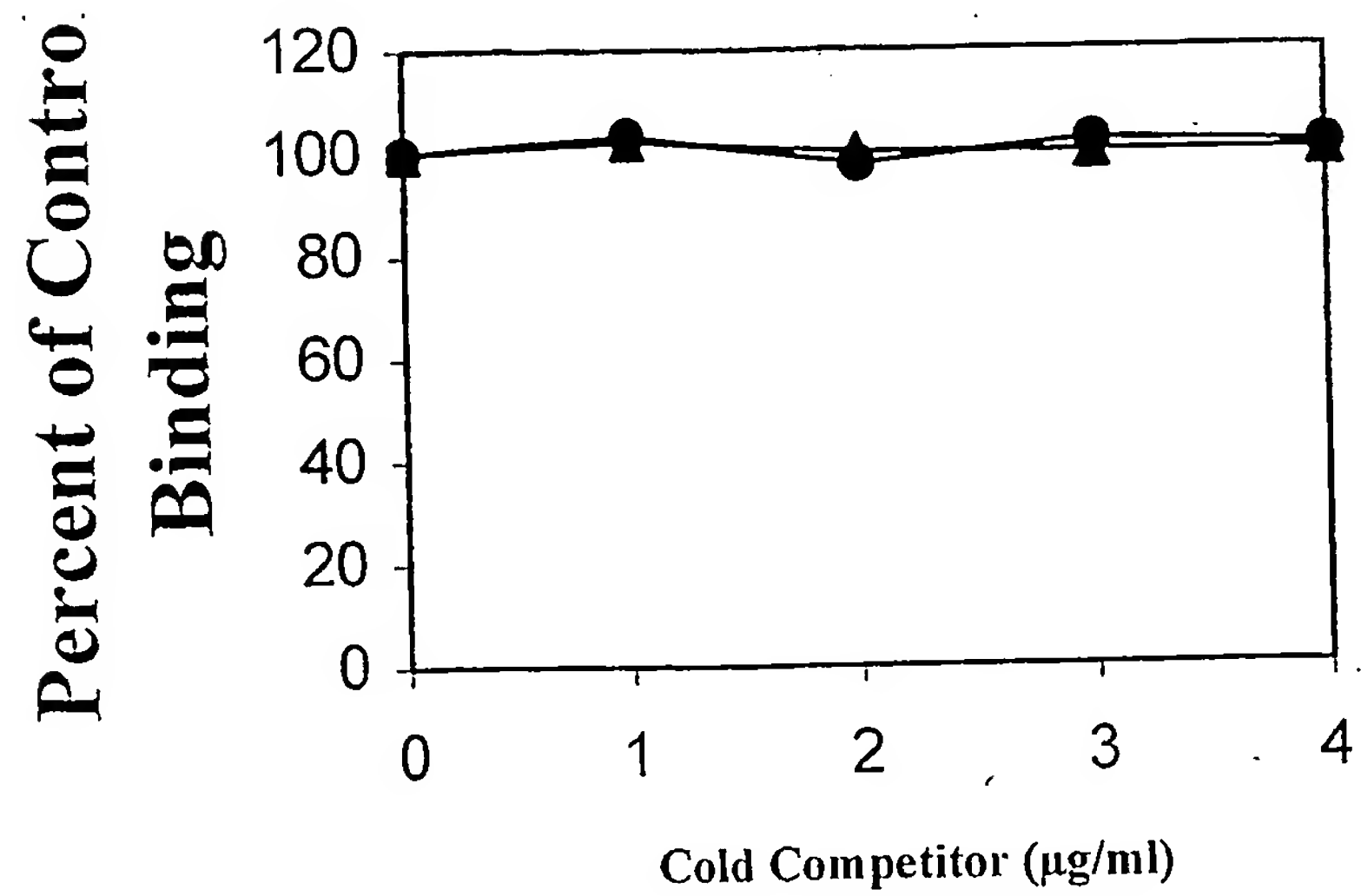
Figures 5A - 5B**A****B**

Figure 6

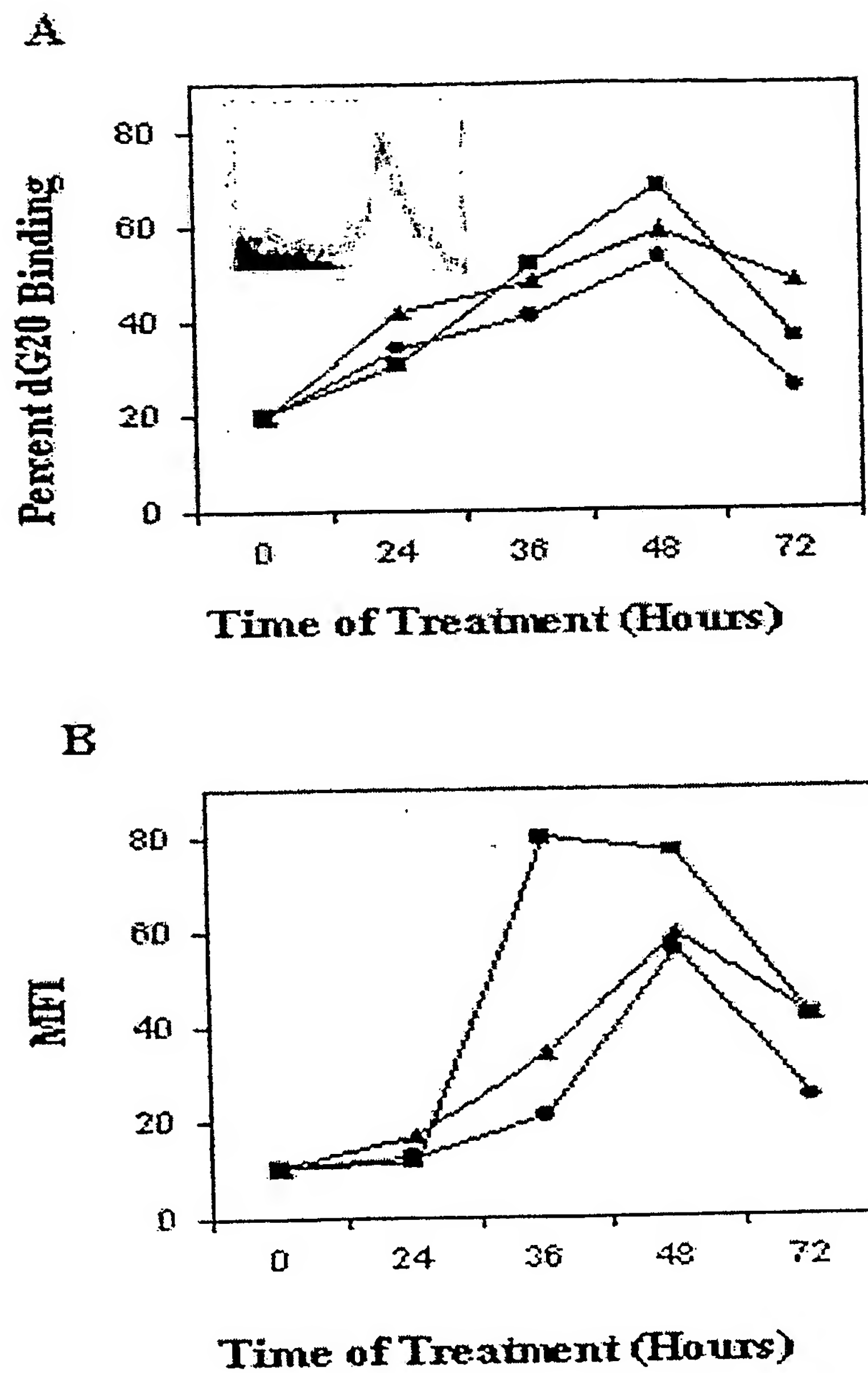


Figure 7

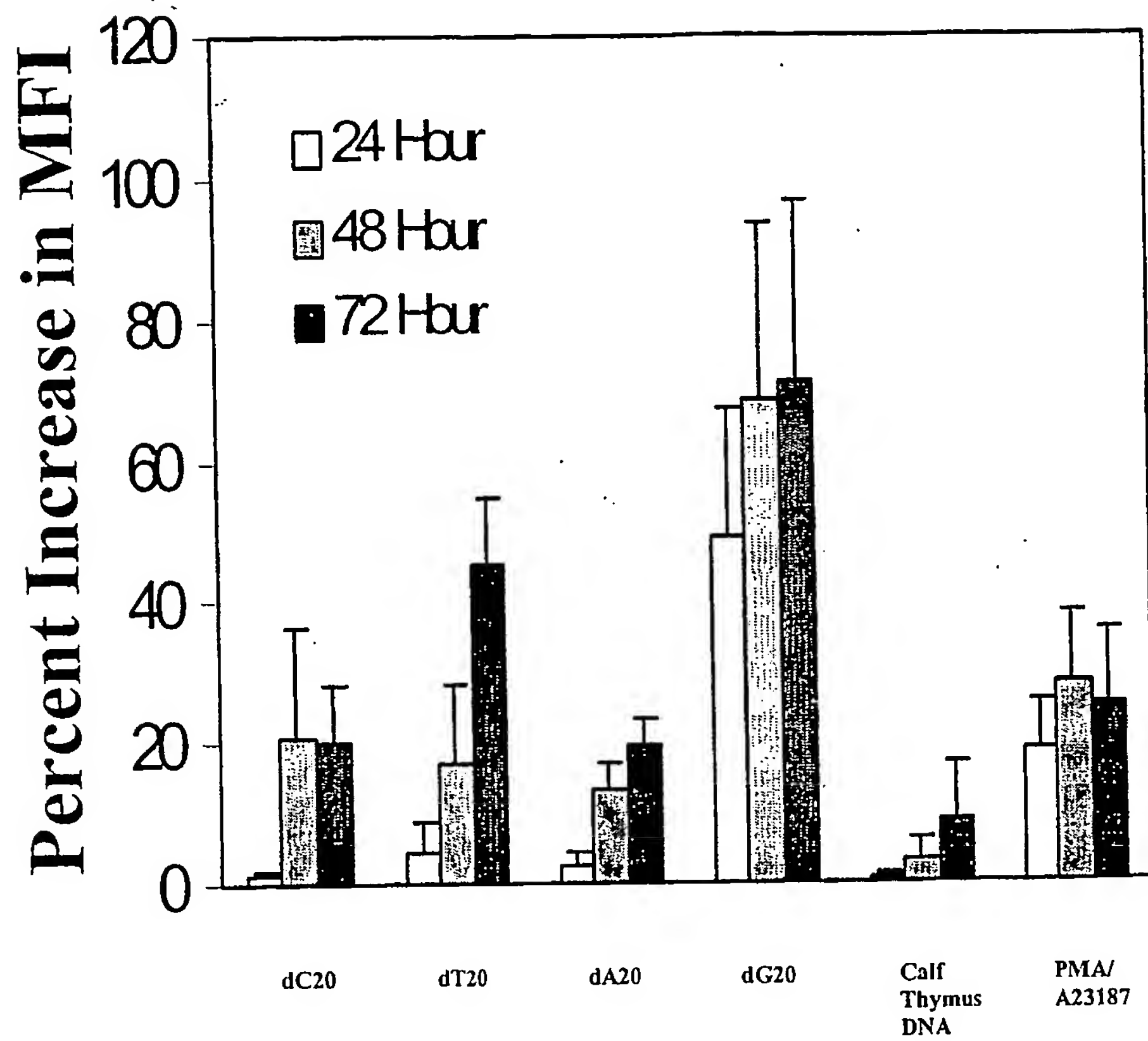
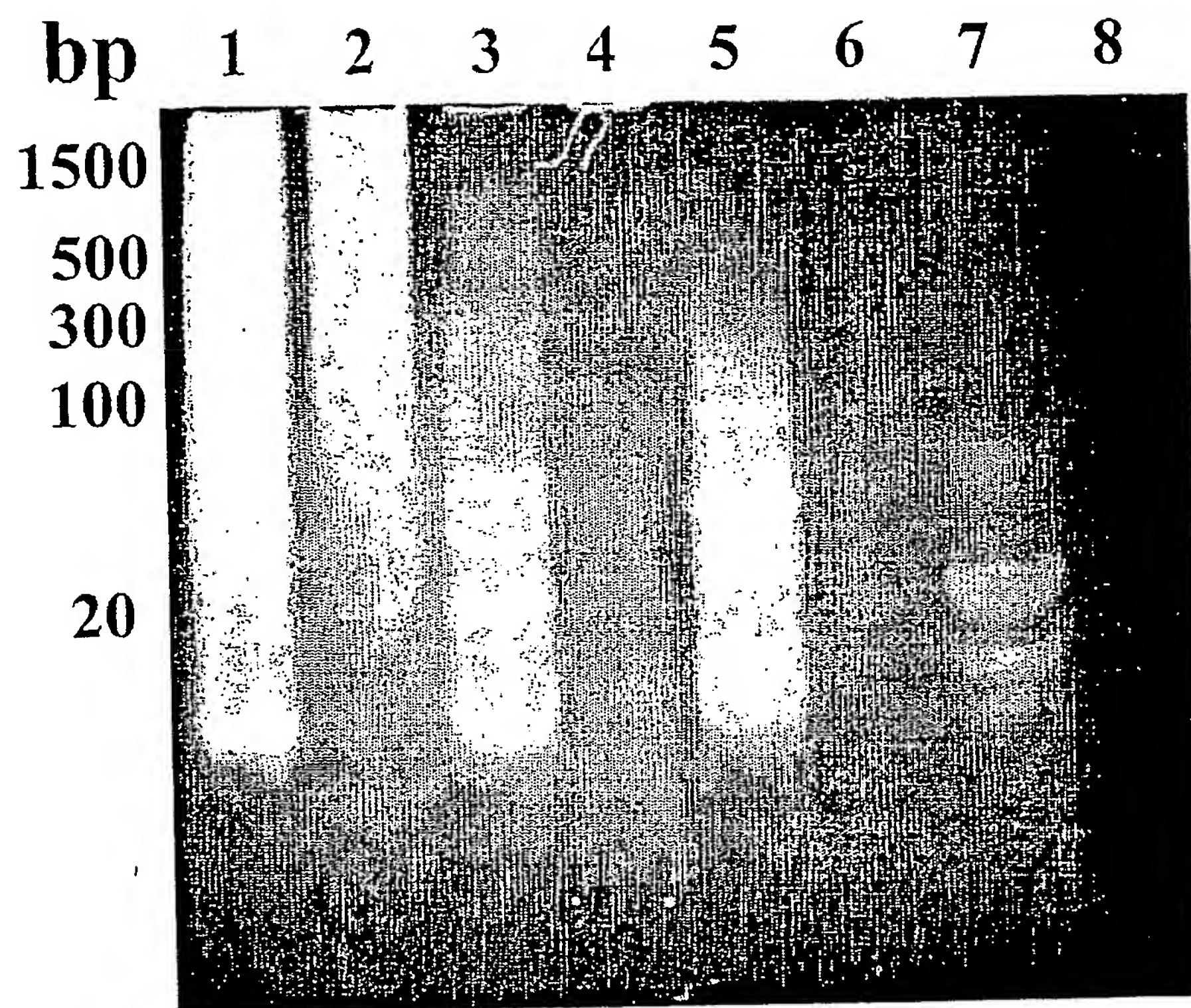


Figure 8



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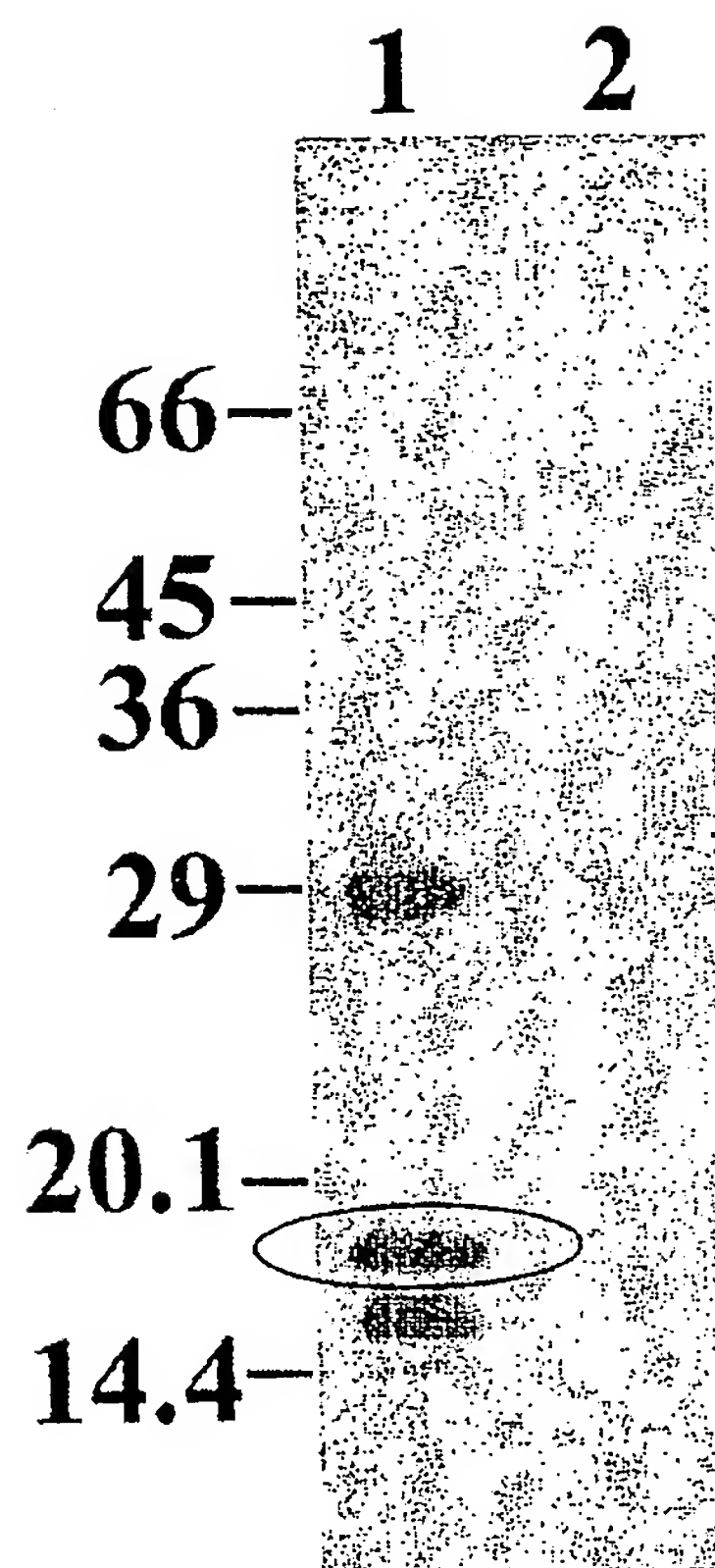
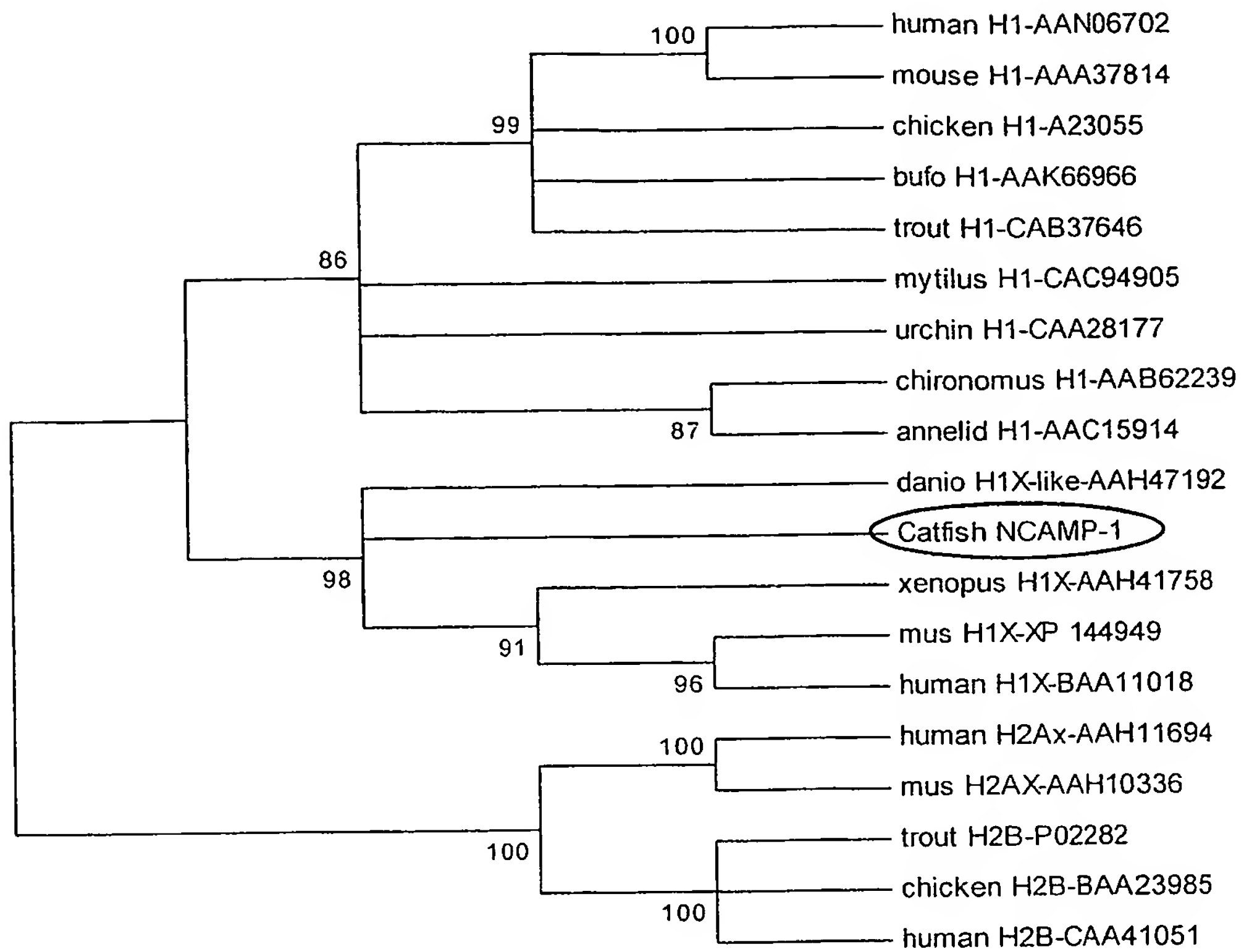
Figure 9**BEST AVAILABLE COPY**

Figure 10

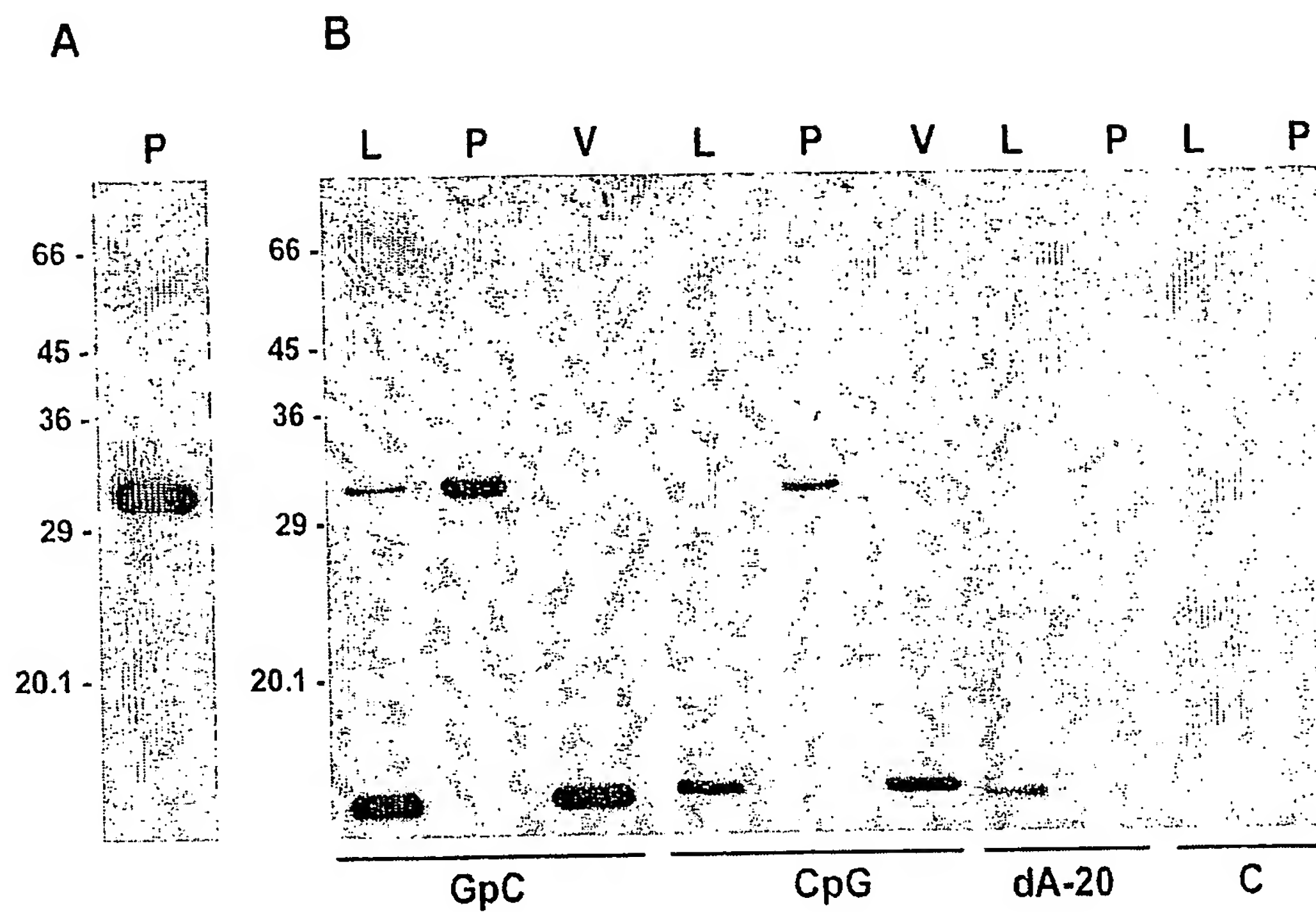
1 CGGCACGAGGGTTCAATAGCATCTCAAGGCGCTTCAGAACTTAAAGTTGA
M S A Q A E E T A P E A A A P V 16
51 ACCATGTCTGCTCAGGCTGAGGAAACTGCACCAGAAGCAGCAGCACCAGT
Q P S Q P A A K K K G P A S K A 32
101 ACAACCATCACAACCAGCGGCCAAAAAGAAGGGACCCGCCAGTAAAGCAA
K P A S A E K K N K K K G K G P 49
151 AGCCTGCCTCTGCAGAAAAAAGAACAAGAAAGGAAAGGGGAAAGGGCCC
G K Y S Q L V I N A I Q T L G E R 66
201 GGAAAGTACAGCCAGCTGGTGATCAATGCTATCCAAACGCTGGGAGAGAG
N G S S L F K I Y N E A K K V N 82
251 AAACGGCTCGTCTCTTTTAAAGATCTACAACGAGGCGAAGAAAGTGAAGT
W F D Q Q H G R V Y L R Y S I R A 99
301 GGTTTGACCAGCAGCAGCGGGCGCGTGTACCTCCGCTACTCCATCCGCGCG
L L Q N D T L V Q V K G L G A N G 116
351 CTGCTGCAGAACGACACGCTCGTGCAGGTGAAGGGTCTGGGCGCCAACGG
S F K L N K K K F I P R T K K S 132
401 CTCCTTCAAGCTCAACAAAAAGAAGTTCATCCCCAGAACCAAGAAGAGCT
S V K P R K T A K P T K K P A K K 149
451 CTGTAAAGCCGAGAAAGACTGCGAAACCGACCAAAAAGCCAGCCAAAAAA
A A K K K K R V S G V K K A T P P 166
501 GCAGCGAAGAAGAAGAAAAGGGTCAGCGGCGTGAAGAAGGCGACTCCCCC
P E K T S K P K K A D K S P A V 182
551 CCCAGAGAAAACCTCCAAACCAAGAAAGCGGATAAAAGTCCAGCCGTCT
S A K K A S K P K K A K Q T K K T 199
601 CTGCCAAGAAGGCGAGCAAGCCCAAGAAAGCTAAACAGACAAAAAAGACT
A K K T * 203
651 GCTAAGAAGACTTAAACGTTTATATTCTGCATGCTTTGTGCATTAAGCA
701 TTGCACTGCGGGTAAACTGCACGCTTTCTGATCGCAGTTCATTAAGTAGG
751 ATATGCACAGTGTTTAACCAAGTGTGCAAGTCACTCTGGTCTCAATGTTT
801 TACTGATGTAACCACATGTAAATAACTGTACAAAGAAGGAAACAATCACT
851 TTTGTAACGTCTGCTTTGTTATTATTTCTTTTCTACTAGTTAGCTAAAAT
901 AACTGCTTATGGCTTCTTTTAAATATATGATAAAAGAAAAA
951 AAAAAA

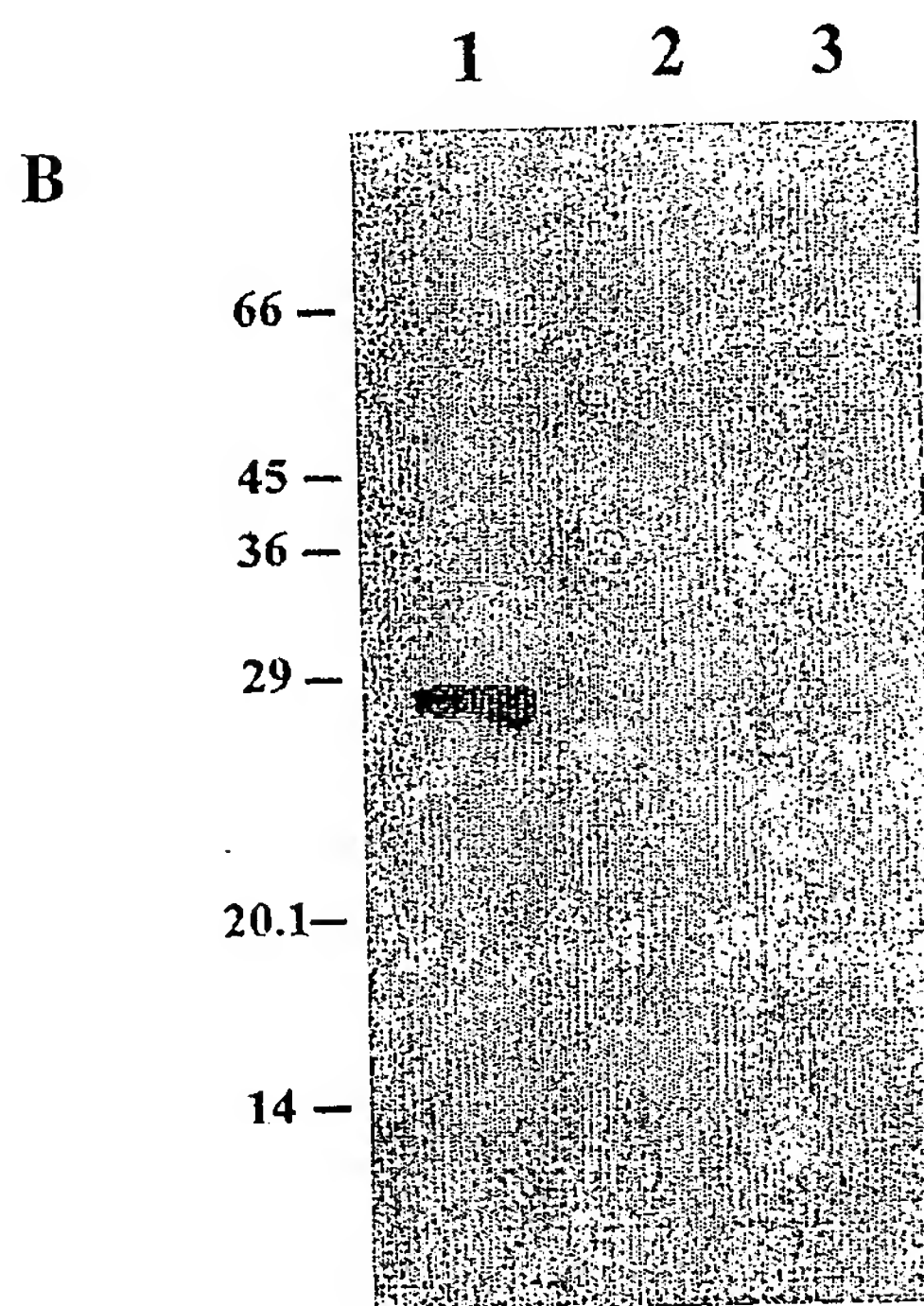
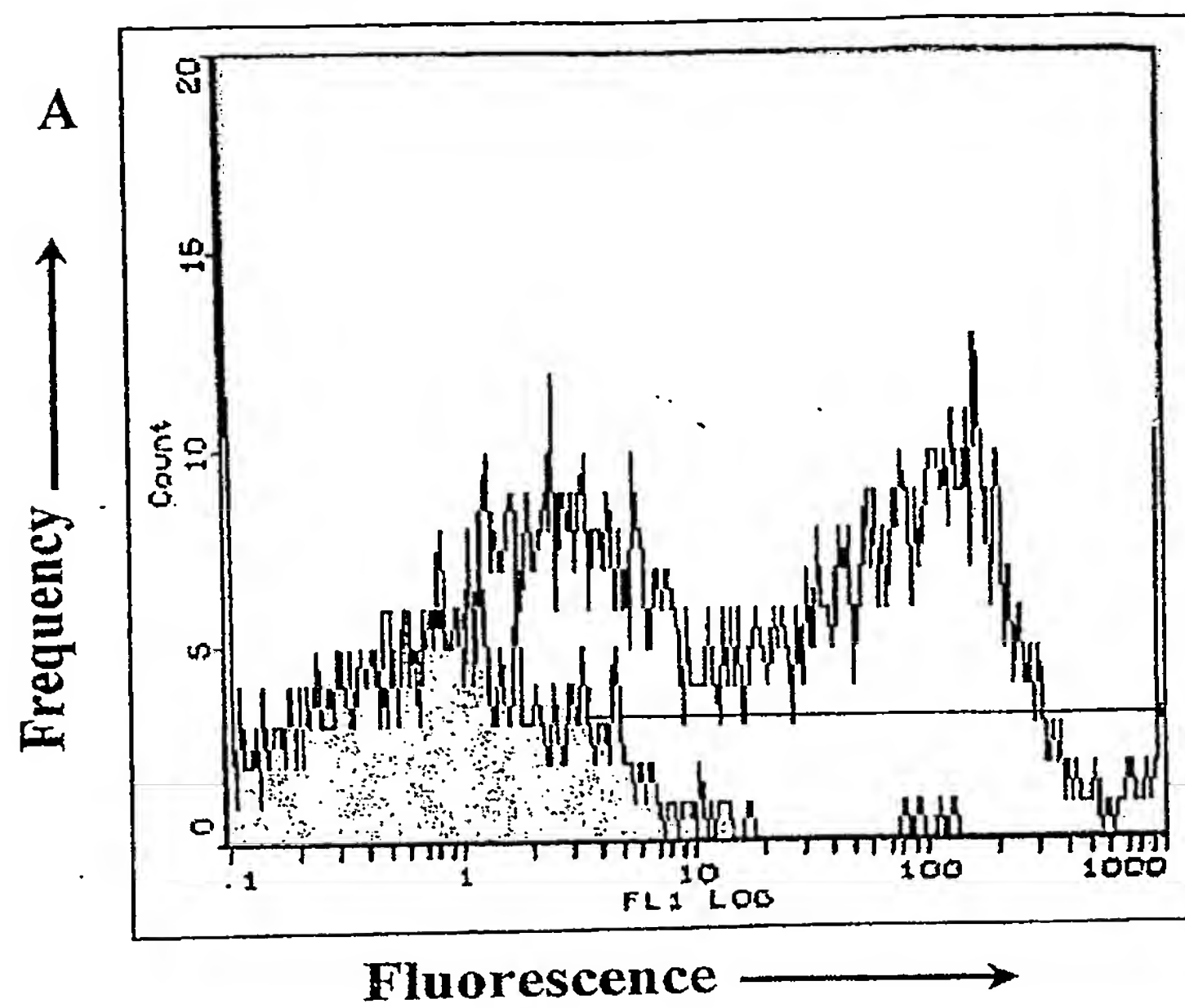
Figure 11

Catfish NCAMP-1	MSAQAEETAP	EAAPVQSPQ	-----AAKKGPASAK	KPASA	EKKKKKKKK	GKGGKYS	CLVINA	QTLGERNG	: 68
Danio H1X-like-AAH47192	-----MPAVVE	ESAPAPAP	-----AEKKAKPAVA	SPAKK	-----KKKKSKG	PGKYS	CLVTD	IRTLGERNG	: 59
Xenopus H1X-AAH41758	-----MALELE	ENLHSTEE	DEEEDE	DEE	DEE	DEE	DEE	DEE	: 73
Mus H1X XP_144949	-----MSVELE	EEALPPTS	ADG	-----TARKTAKAGG	SAAPTQ	PKRRKN	PKKNQ	PGKYS	: 63
human H1X-BAA11018	-----MSVELE	EEALPVT	TAEG	-----MAKKVT	KAGGSA	ALSPSK	RRKN	SKKNQ	: 64
Catfish NCAMP-1	SSLEKIIYNE	EAKKVN	MEDQ	QHGRV	YLRYS	STRALV	NDTLVQVKG	GANGSEKLN	: 148
Danio H1X-like-AAH47192	SSLEKIIYNE	EAKKVN	MEDQ	KNGRM	YLRYS	STRALV	NDTLVQVKG	GANGSEKLN	: 138
Xenopus H1X-AAH41758	SSLEKIIYNE	EAKKVN	MEDQ	QNGRT	YLRYS	STRALV	NDTLVQVKG	GANGSEKLN	: 153
Mus H1X XP_144949	SSLEKIIYNE	EAKKVN	MEDQ	QNGRT	YLRYS	STRALV	NDTLVQVKG	GANGSEKLN	: 140
human H1X-BAA11018	SSLEKIIYNE	EAKKVN	MEDQ	QNGRT	YLRYS	STRALV	NDTLVQVKG	GANGSEKLN	: 144
Catfish NCAMP-1	KAAC-----	KKKRVSGV	KKAT	PPPE	TSKPK	-----KADKSP	AVSAK	SRPKRAK	: 203
Danio H1X-like-AAH47192	KAVT-----	KKVS	AKKSAK	SPVKK	MTPKKT	-----SVKKAT	AKPKKT	ASKKP	: 192
Xenopus H1X-AAH41758	QQQ-----	GPSSSP	SKSHK	AKPKA	KAEEK	EKPKT	SSAKA	SPKSAK	: 217
Mus H1X XP_144949	-----TAAADR	TPAR	PQ	-----PER	RAHKS	-----KKA	AAA	ASAK	: 188
human H1X-BAA11018	KKAAPGA	AGSRR	ADKKPAR	GQKPE	QRSHK	KGAGAK	KDKG	AKKAAK	: 213

Figure 12

Figures 13A - 13B



Figures 14A - 14B**BEST AVAILABLE COPY**

Figures 15A - 15B

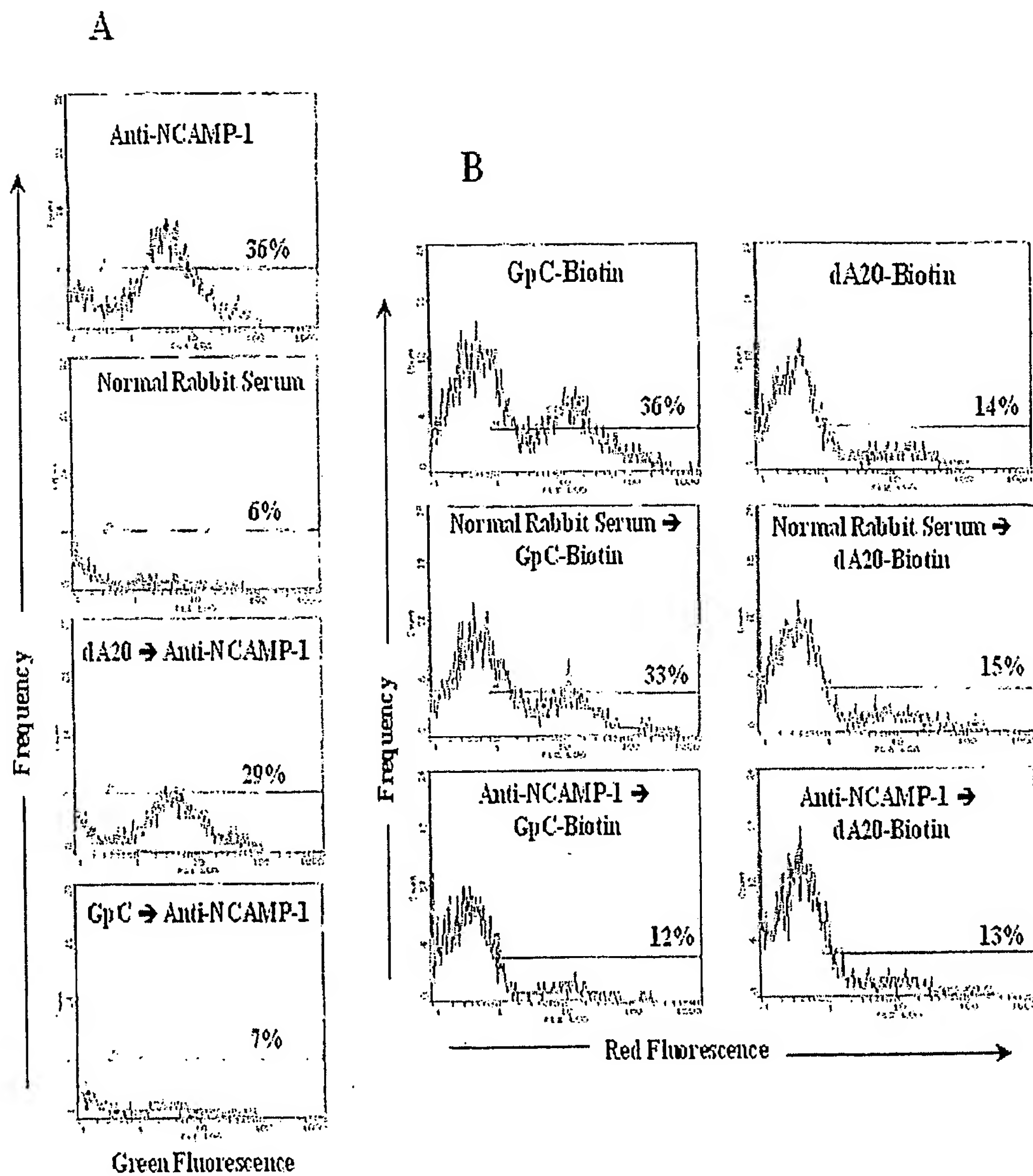


FIGURE 16

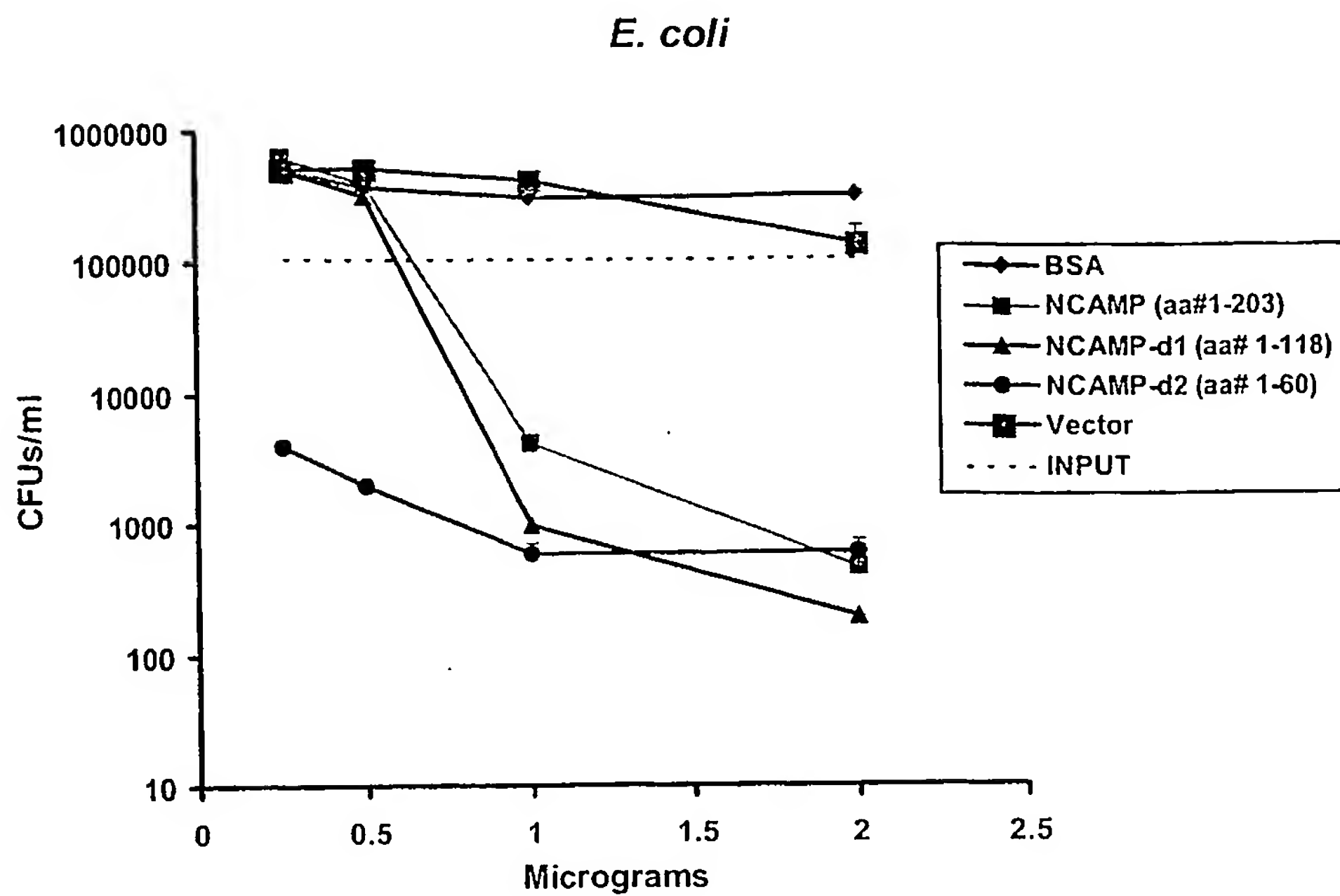
NCAMP-1 PEAAAPVQPSQPAAKKKGPASKAKPASAEKKNKKAKGKGPG
 H1-Mus -----SETAPAEKPAKPAKAE--
 H1-Human ----KLNKKAAASGEAKPKAKAKSPKKAKA--
 H1-Trout -KAVAAKKSPKKAKKPAT--

C-Terminal residues :

NCAMP-1
 -TAKPTKKPAKKAACKKKRVSGVKKATPPPEKTSKPKKADKSPAVSAKKASKPKKAKQT
 H2A CF --KGRGKQGGKVRAKAKTRSS--
 H2B Trout -----PDPAKTAPKKGSKKAVTKXA--
 H2B Bass1 -----PEPAKSAPKKGSKKAVT-
 H2B Bass2 -----PDPAKTAPKKGSKKAVTKTAG
 H1-Trout -----AEVAPAPAAAPAKAPKKKA
 H1-Trout ---AEVAPAPAAAPAKAPKKKAAAKPKK-----

Figures 17A - 17B

A



B

